

<110> Duvick, Jonathan P.  
Gilliam, Jacob T.  
Maddox, Joyce R.  
Crasta, Oswald R.  
Folkerts, Otto

<130> 0875C

<151> 1998-07-15

<151> 1999-07-12

<160> 33

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<170> FastSEQ for Windows Version 3.0
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<212> DNA

<213> Exophiala spinifera.

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<221> misc feature

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ggaggacgcc	cgagaagcct	tgttcgcgcc	accacggctt	gtcccatacag	aagactatct	240
tgctatagta	gcccaggata	gaattttccg	ccaatgcttg	cttctcggcg	ggaagaggtg	300
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<213> *Exophiala spinifera*.

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ac                                              182
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<211> 29

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<213> Artificial Sequence

**<220>**

<223> Designed oligonucleotide for 3' RACE, N21965

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tggtttcggtt accgacaacc ttgtatccc

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<210> 4

<211> 28

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<223> Designed oligonucleotide for 5' RACE, N21968

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<213> *Exophiala spinifera*

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48

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt  
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30

96

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt  
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

144

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac  
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

192

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag  
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

240

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac  
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

288

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag  
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

336

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc  
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

384

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg  
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

432

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Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	
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cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggc	528
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gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	
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Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	
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Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	
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Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	
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385											390											395											400											
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Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly																													
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
          20          25          30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt      144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
          35          40          45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac      192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
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Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
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ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac      288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
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Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
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ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgctcgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	
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tcgtttctca gtggtcattc cag gt atg cag tcg att tgc cat gcc atg tca	728
Gly Met Gln Ser Ile Cys His Ala Met Ser	
220 225	
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Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
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att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
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Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
290 295 300 305	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	1064

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ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	1208	
Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala		
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Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala		
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ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	1304	
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala		
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ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	1352	
Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser		
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tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga	1400	
Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg		
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ggt	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	tag			1442	
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Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	
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Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	
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 165 170 175  
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
 180 185 190  
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
 195 200 205  
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
 210 215 220  
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
 225 230 235 240  
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
 245 250 255  
 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu  
 260 265 270  
 Tyr Pro Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln Ala  
 275 280 285  
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
 290 295 300  
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
 305 310 315 320  
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 325 330 335  
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 340 345 350  
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
 355 360 365  
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
 370 375 380  
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
 385 390 395 400  
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
 405 410 415  
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
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<212> PRT

<213> *Exophiala spinifera*

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 35 40 45  
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60  
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 65 70 75 80  
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
 85 90 95  
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
 100 105 110  
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
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 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg

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 165 170 175  
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
 180 185 190  
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
 195 200 205  
 Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly  
 210 215 220  
 Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met  
 225 230 235 240  
 Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro  
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 Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro  
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 275 280 285  
 Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys  
 290 295 300  
 His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr  
 305 310 315 320  
 Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn  
 325 330 335  
 Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser  
 340 345 350  
 Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly  
 355 360 365  
 Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr  
 370 375 380  
 Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg  
 385 390 395 400  
 Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu  
 405 410 415  
 Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg  
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 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
 <221> CDS  
 <222> (1)...(1389)  
 <221> misc\_feature  
 <222> (1)...(3)  
 <223> Extra lysine in K:trAPAO

<400> 10

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 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
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48

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val

96

20					25					30						
ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	144
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	
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ggg	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	192
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
	50					55					60					
gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	240
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	
65					70					75					80	
gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	288
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	
				85					90					95		
gac	ggg	aca	acc	act	aca	gct	cct	tat	ggg	gac	tcc	ttg	ctg	agc	gag	336
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
			100					105					110			
gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	384
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	
		115					120					125				
atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	432
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	
	130					135					140					
cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	480
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	
145					150					155					160	
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Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	
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ggg	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	576
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	
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aag	agt	gcc	acc	ggg	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	624
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	
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Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	
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atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	720
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	
225					230					235					240	
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	768
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	
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ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	816
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	
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<211> 463
<212> PRT
<213> Exophiala spinifera

<220>
<223> Extra lysine in the polypeptide sequence of
      K:trAPAO, 463 aa.

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 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
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 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
                   50                  55                  60  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
                   65                  70                  75                  80  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
                   85                  90                  95  
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
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 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
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 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
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 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
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 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
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 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
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                   245                  250                  255  
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
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 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
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 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
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 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
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 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
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 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
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 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
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 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
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 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
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 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
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 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
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 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
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 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
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&lt;210&gt; 12

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer sequence designed for cloning DNA into  
 expression vectors, N23259

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 <212> DNA  
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 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

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 <213> *Exophiala spinifera*

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 <222> (1)...(267)  
 <223> yeast alpha mating factor secretion signal.

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 <222> (1)...(1662)

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gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96  
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln  
 -70 -65 -60

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		-55				-50						-45				
gat Asp	gtt Val	gct Ala	gtt Val	ttg Leu	cca Pro	ttt Phe	tcc Ser	aac Asn	agc Ser	aca Thr	aat Asn	aac Asn	ggg Gly	tta Leu	ttg Leu	192
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ttt Phe	ata Ile	aat Asn	act Thr	act Thr	att Ile	gcc Ala	agc Ser	att Ile	gct Ala	gct Ala	aaa Lys	gaa Glu	gaa Glu	ggg Gly	gta Val	240
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tct Ser	ctc Leu	gag Glu	aaa Lys	aga Arg	gag Glu	gct Ala	gaa Glu	gct Ala	gaa Glu	ttc Phe	aaa Lys	gac Asp	aac Asn	gtt Val	gcg Ala	288
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aaa Lys	gtc Val	cag Gln	gcc Ala	gcc Ala	ggg Gly	ctg Leu	tcc Ser	tgc Cys	ctc Leu	gtt Val	ctt Leu	gag Glu	gcg Ala	atg Met	gat Asp	384
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cgt Arg	gta Val	ggg Gly	gga Gly	aag Lys	act Thr	ctg Leu	agc Ser	gta Val	caa Gln	tcg Ser	ggg Gly	ccc Pro	ggc Gly	agg Arg	acg Thr	432
40				45						50						55
act Thr	atc Ile	aac Asn	gac Asp	ctc Leu	ggc Gly	gct Ala	gcg Ala	tgg Trp	atc Ile	aat Asn	gac Asp	agc Ser	aac Asn	caa Gln	agc Ser	480
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gaa Glu	gta Val	tcc Ser	aga Arg	ttg Leu	ttt Phe	gaa Glu	aga Arg	ttt Phe	cat His	ttg Leu	gag Glu	ggc Gly	gag Glu	ctc Leu	cag Gln	528
		75						80				85				
agg Arg	acg Thr	act Thr	gga Gly	aat Asn	tca Ser	atc Ile	cat His	caa Gln	gca Ala	caa Gln	gac Asp	ggg Gly	aca Thr	acc Thr	act Thr	576
		90				95						100				
aca Thr	gct Ala	cct Pro	tat Tyr	ggg Gly	gac Asp	tcc Ser	ttg Leu	ctg Leu	agc Ser	gag Glu	gag Glu	gtt Val	gca Ala	agt Ser	gca Ala	624
		105				110						115				
ctt Leu	gcg Ala	gaa Glu	ctc Leu	ctc Leu	ccc Pro	gta Val	tgg Trp	tct Ser	cag Gln	ctg Leu	atc Ile	gaa Glu	gag Glu	cat His	agc Ser	672
120				125						130				135		
ctt Leu	caa Gln	gac Asp	ctc Leu	aag Lys	gcg Ala	agc Ser	cct Pro	cag Gln	gcg Ala	aag Lys	cg Arg	ctc Leu	gac Asp	agt Ser	gtg Val	720
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agc Ser	ttc Phe	gcg Ala	cac His	tac Tyr	tgt Cys	gag Glu	aag Lys	gaa Glu	cta Leu	aac Asn	ttg Leu	cct Pro	gct Ala	gtt Val	ctc Leu	768
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Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	
185						190					195					
ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	912
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	
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Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	
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gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	1008
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	
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Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	
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agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	1104
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	
	265					270					275					
aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	1152
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	
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tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	1200
Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	
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Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	
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ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	1296
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	
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Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	
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Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	
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Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	
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gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	1488
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	
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gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	ctc	aga	acg	1536
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	
		410					415					420				
ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	1584
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	
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aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca 1632  
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala  
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gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c 1673  
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<210> 17  
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 <213> *Exophiala spinifera*

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 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
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 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
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 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala  
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 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg  
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 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp  
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 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr  
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 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser  
 60 65 70  
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln  
 75 80 85  
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr  
 90 95 100  
 Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala  
 105 110 115  
 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser  
 120 125 130 135  
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 140 145 150  
 Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu  
 155 160 165  
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His  
 170 175 180  
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly  
 185 190 195  
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gln Tyr Met Arg  
 200 205 210 215  
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu  
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 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln

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Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu
	265					270					275				
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn
280					285					290					295
Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro
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Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp
			315					320					325		
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp
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Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln
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Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala
360					365					370					375
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu
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Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala
			395					400					405		
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr
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Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp
	425					430					435				
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala
440					445					450					455
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala						
				460				465							

<210>	18
<211>	2079
<212>	DNA
<213>	Unknown

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<221> CDS  
<222> (1) ... (2076)
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<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1  
- 687, gst fusion + polylinker; 688-2076,  
K:trAPAO; 2077-2079, stop codon. For bacterial  
expression.

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<221> misc_feature
<222> (1)...(687)
<223> gst fusion + polylinker
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<221> misc_feature
<222> (688)...(2076)
<223> K:trAPAO
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<221> misc_feature
<222> (688)...(690)
<223> Extra lysine
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Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5					10					15		
act	cga	ctt	ctt	ttg	gaa	tat	ctt	gaa	gaa	aaa	tat	gaa	gag	cat	ttg	96

Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	gtt	aaa	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
	65				70				75						80	
atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85				90						95		
gga	gcg	ggt	ttg	gat	att	aga	tac	ggt	ggt	tcg	aga	att	gca	tat	agt	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
aaa	gac	ttt	gaa	act	ctc	aaa	ggt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
	145				150					155				160		
ggt	ggt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165				170						175		
ggt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
acg	ttt	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	ggt	ccg	cgt	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
gga	tcc	ccg	gaa	ttc	aaa	gac	aac	ggt	gcg	gac	gtg	gta	gtg	gtg	ggc	720
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	
	225				230					235					240	
gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggt	768
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	
				245				250					255			
ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	816
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	
			260					265					270			

ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc	864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	
275 280 285	
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt	912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	
290 295 300	
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca	960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser	
305 310 315 320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac	1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp	
325 330 335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc	1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	
340 345 350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
355 360 365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
370 375 380	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc	1200
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
385 390 395 400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	
405 410 415	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg	1296
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
515 520 525

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc 1632  
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Arg Glu Gln Gly  
530 535 540

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga 1680  
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
545 550 555 560

gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg 1728  
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
565 570 575

gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga 1776  
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
580 585 590

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg 1824  
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
595 600 605

gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag 1872  
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
610 615 620

cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat 1920  
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
625 630 635 640

ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat 1968  
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
645 650 655

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg 2016  
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
660 665 670

gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg 2064  
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
675 680 685

gtg cca gca gca tag 2079  
Val Pro Ala Ala  
690

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230-692

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Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
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Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50				55					60					
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75					80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100					105					110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
	115						120					125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135					140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155					160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165				170						175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180					185					190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
	195						200					205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215					220				
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly
225					230					235					240
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly
				245					250					255	
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr
			260					265					270		
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly
		275					280					285			
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe
	290					295					300				
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser
305					310					315					320
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp
				325					330					335	
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro
			340					345					350		
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala
		355					360					365			
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys
	370					375					380				
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile
385					390					395					400
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe
				405					410					415	
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser
		420						425					430		
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln
		435					440					445			
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His
	450					455					460				
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr
465					470					475					480
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val
				485					490					495	
Ser	Leu	Pro	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	
			500					505					510		
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr
		515					520						525		

09770664 043604

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
 530 535 540  
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
 545 550 555 560  
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
 565 570 575  
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
 580 585 590  
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
 595 600 605  
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
 610 615 620  
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
 625 630 635 640  
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
 645 650 655  
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
 660 665 670  
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
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 Val Pro Ala Ala  
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 <213> Unknown  
  
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 <222> (1)...(72)  
 <223> Barley Alpha Amylase signal sequence.

<221> misc\_feature  
 <222> (73)...(1464)  
 <223> K:trAPAOcDNA

<221> CDS  
 <222> (1)...(1461)

<223> Nucleotide sequence of K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464 , trAPAO cDNA.

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 <222> (73)...(75)  
 <223> Added lysine residue

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 -20 -15 -10  
  
 ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta 96  
 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
 -5 1 5  
  
 gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag 144  
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

0970664.04.0504

10				15				20								
gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	ggg	192
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	
25					30					35					40	
gga	aag	act	ctg	agc	gta	caa	tgc	ggt	ccc	ggc	agg	acg	act	atc	aac	240
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	
				45					50					55		
gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	tcc	288
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	
			60					65					70			
aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	act	336
Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	
		75					80					85				
gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	cct	384
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	
	90					95					100					
tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	ggt	gca	agt	gca	ctt	gcg	gaa	432
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	
105					110					115					120	
ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	gac	480
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	
				125					130					135		
ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc	gcg	528
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	
			140					145					150			
cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	gca	576
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	
		155					160					165				
aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	gtg	gaa	gcc	cac	gag	atc	agc	624
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	
	170					175					180					
atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggt	ctc	agt	aat	672
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	
185					190					195					200	
att	ttc	tgc	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	aca	720
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	
				205					210					215		
ggt	atg	cag	tgc	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	ggc	768
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	
			220					225					230			
tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tgc	gca	tcc	816
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	
		235					240					245				
ggc	tgt	aca	gta	cga	tgc	gcc	tgc	ggc	gcc	gtg	ttc	cga	agc	aaa	aag	864
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	
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<213> Unknown

<220>
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<222> (1) ... (24
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<223> K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize.

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Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
-5 1 5  
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
10 15 20  
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
25 30 35 40  
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
45 50 55  
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
60 65 70  
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
75 80 85  
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro  
90 95 100  
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
105 110 115 120  
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp  
125 130 135  
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Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
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Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys  
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tcc Ser	aga Arg	ttg Leu	ttt Phe	gaa Glu	aga Arg	ttt Phe	cat His	ttg Leu	gag Glu	ggc Gly	gag Glu	ctc Leu	cag Gln	agg Arg	acg Thr	1872
act Thr	gga Gly	aat Asn	tca Ser	atc Ile	cat His	caa Gln	gca Ala	caa Gln	gac Asp	ggg Gly	aca Thr	acc Thr	act Thr	aca Thr	gct Ala	1920
cct Pro	tat Tyr	ggg Gly	gac Asp	tcc Ser	ttg Leu	ctg Leu	agc Ser	gag Glu	gag Glu	gtt Val	gca Ala	agt Ser	gca Ala	ctt Leu	gcg Ala	1968
gaa Glu	ctc Leu	ctc Leu	ccc Pro	gta Val	tgg Trp	tct Ser	cag Gln	ctg Leu	atc Ile	gaa Glu	gag Glu	cat His	agc Ser	ctt Leu	caa Gln	2016
gac Asp	ctc Leu	aag Lys	gcg Ala	agc Ser	cct Pro	cag Gln	gcg Ala	aag Lys	cgg Arg	ctc Leu	gac Asp	agt Ser	gtg Val	agc Ser	ttc Phe	2064
gcg Ala	cac His	tac Tyr	tgt Cys	gag Glu	aag Lys	gaa Glu	cta Leu	aac Asn	ttg Leu	cct Pro	gct Ala	gtt Val	ctc Leu	ggc Gly	gta Val	2112
gca Ala	aac Asn	cag Gln	atc Ile	aca Thr	cgc Arg	gct Ala	ctg Leu	ctc Leu	ggg Gly	gtg Val	gaa Glu	gcc Ala	cac His	gag Glu	atc Ile	2160
agc Ser	atg Met	ctt Leu	ttt Phe	ctc Leu	acc Thr	gac Asp	tac Tyr	atc Ile	aag Lys	agt Ser	gcc Ala	acc Thr	ggg Gly	ctc Leu	agt Ser	2208
aat Asn	att Ile	ttc Phe	tcg Ser	gac Asp	aag Lys	aaa Lys	gac Asp	ggc Gly	ggg Gly	cag Gln	tat Tyr	atg Met	cga Arg	tgc Cys	aaa Lys	2256
aca Thr	ggg Gly	atg Met	cag Gln	tcg Ser	att Ile	tgc Cys	cat His	gcc Ala	atg Met	tca Ser	aag Lys	gaa Glu	ctt Leu	gtt Val	cca Pro	2304
ggc Gly	tca Ser	gtg Val	cac His	ctc Leu	aac Asn	acc Thr	ccc Pro	gtc Val	gct Ala	gaa Glu	att Ile	gag Glu	cag Gln	tcg Ser	gca Ala	2352
tcc Ser	ggc Gly	tgt Cys	aca Thr	gta Val	cga Arg	tcg Ser	gcc Ala	tcg Ser	ggc Gly	gcc Ala	gtg Val	ttc Phe	cga Arg	agc Ser	aaa Lys	2400
aag Lys	gtg Val	gtg Val	gtt Val	tcg Ser	tta Leu	ccg Pro	aca Thr	acc Thr	ttg Leu	tat Tyr	ccc Pro	acc Thr	ttg Leu	aca Thr	ttt Phe	2448
tca Ser	cca Pro	cct Pro	ctt Leu	ccc Pro	gcc Ala	gag Glu	aag Lys	caa Gln	gca Ala	ttg Leu	gcg Ala	gaa Glu	aat Asn	tct Ser	atc Ile	2496
ctg Leu	ggc Gly	tac Tyr	tat Tyr	agc Ser	aag Lys	ata Ile	gtc Val	ttc Phe	gta Val	tgg Trp	gac Asp	aag Lys	ccg Pro	tgg Trp	tgg Trp	2544

<400> 25															
Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
				-20					-15					-10	
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala
				-5					1					5	
Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr
		10					15					20			
Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe
25					30					35					40
Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr

**DO NOT WRITE IN THESE SPACES**

**SECRET**

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<210> 26
<211> 2976
<212> DNA
<213> Unknown

<220>
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<223> Barley alpha amylase signal sequence: BEST1  
mature: artificial spacer: and K:trAPAO. For  
plant expression.

<221> sig\_peptide

<222> (1)...(72)

<223> Barley alpha amylase signal sequence.

<221> mat\_peptide

<222> (73)...(1545)

<223> BEST1 mature

<221> misc\_feature

<222> (1546)...(1584)

<223> Artificial spacer sequence

<221> misc\_feature

<222> (1585)...(2973)

<223> K:trAPAO

<221> CDS

<222> (1)...(2973)

<221> misc\_feature

<222> (1585)...(1587)

<223> Extra lysine

<400> 26

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly	
-20 -15 -10	
ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc	96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr	
-5 1 5	
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc	144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	
10 15 20	
gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg	192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	
25 30 35 40	
ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt	240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	
45 50 55	
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc	288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	
60 65 70	
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca	336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	
75 80 85	
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc	384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
90 95 100	
ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg	432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	

105	110	115	120	
ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	125	130	135	480
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	140	145	150	528
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg	155	160	165	576
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	170	175	180	624
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	185	190	195	672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	205	210	215	720
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	220	225	230	768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	235	240	245	816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	250	255	260	864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	265	270	275	912
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val	285	290	295	960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly	300	305	310	1008
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala	315	320	325	1056
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp	330	335	340	1104
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn	345	350	355	1152
				360

00770564 043604

cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag	1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln	
365 370 375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly	
380 385 390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc	1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	
425 430 435 440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct	1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro	
445 450 455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc	1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	
460 465 470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc	1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	
475 480 485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc	1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	
490 495 500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
505 510 515 520	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
525 530 535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
540 545 550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
555 560 565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
570 575 580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
585 590 595 600	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	

				605				610				615							
gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	1968			
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu				
620								625				630							
atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	2016			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys				
635								640				645							
cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	2064			
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn				
650								655				660							
ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	2112			
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu				
665								670				675				680			
ggc	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	2160			
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile				
685								690				695							
aag	agt	gcc	acc	ggc	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	2208			
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly				
700								705				710							
ggg	cag	tat	atg	cga	tgc	aaa	aca	ggc	atg	cag	tcg	att	tgc	cat	gcc	2256			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala				
715								720				725							
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	2304			
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val				
730								735				740							
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	2352			
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser				
745								750				755				760			
ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	2400			
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr				
765								770				775							
ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	2448			
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln				
780								785				790							
gca	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	2496			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe				
795								800				805							
gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	2544			
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu				
810								815				820							
caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	2592			
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp				
825								830				835				840			
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	2640			
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly				
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<210> 27
<211> 991
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

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Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
      -5                      1                      5
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
      10                      15                      20
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25                      30                      35                      40
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
      45                      50                      55
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
      60                      65                      70
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
      75                      80                      85
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
      90                      95                      100
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
105                      110                      115                      120
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
      125                      130                      135
Ile Leu Gly Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
      140                      145                      150

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Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
650                      655                      660
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665                      670                      675                      680
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
685                      690                      695
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
700                      705                      710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
715                      720                      725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
730                      735                      740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                      750                      755                      760
Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr
765                      770                      775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
780                      785                      790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795                      800                      805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810                      815                      820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                      830                      835                      840
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
845                      850                      855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860                      865                      870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875                      880                      885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
890                      895                      900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                      910                      915                      920
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
925                      930                      935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
940                      945                      950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955                      960                      965

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<210> 28
<211> 3618
<212> DNA
<213> Unknown

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<220>
<223> gst:esp1:sp:K:trapao, 3618. 1-687, gst +
polylinker; 688-2190, esp1 mat; 2191-2226 spacer;
2227-3615, K:trAPAO, extra lysine; 3616-3618, stop
codon. For bacterial expression.

```

```

<221> CDS
<222> (1)...(3615)

<221> misc_feature
<222> (1)...(687)
<223> gast + polylinker

```

```

<221> mat_peptide
<222> (688)...(2190)
<223> esp1 mat

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<221> misc_feature
<222> (2227)...(2229)
<223> Extra lysine
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<400> 28																
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Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5				10				15				
act	cga	ctt	ctt	ttg	gaa	tat	ctt	gaa	gaa	aaa	tat	gaa	gag	cat	ttg	96
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
20				25				30								
tat	gag	cgc	gat	gaa	ggg	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
35				40				45								
ggg	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggg	gat	gtt	aaa	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
50				55				60								
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65				70				75				80				
atg	ttg	ggg	ggg	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
85				90				95								
gga	gcg	gtt	ttg	gat	att	aga	tac	ggg	gtt	tcg	aga	att	gca	tat	agt	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
100				105				110								
aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
115				120				125								
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
130				135				140								
ggg	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145				150				155				160				
gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
165				170				175								
gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
180				185				190								

ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	624					
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Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala	Ala	Phe	Gly						
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Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala	Gly	Gly	Arg						
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Ser	Val	As																			

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gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465 470 475 480			1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495			1488
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acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625 630 635 640			1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645 650 655			1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660 665 670			2016
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Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly	
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Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val	
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Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala	
755 760 765	
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Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys	
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Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu	
785 790 795 800	
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Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu	
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Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn	
820 825 830	
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt	2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly	
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Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu	
850 855 860	
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag	2640
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys	
865 870 875 880	
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac	2688
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr	
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Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln	
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atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt	2784
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu	
915 920 925	
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Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	

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cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val 965 970 975			2928
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys 980 985 990			2976
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val 995 1000 1005			3024
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro 1010 1015 1020			3072
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr 1025 1030 1035 1040			3120
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln 1045 1050 1055			3168
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala 1060 1065 1070			3216
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe 1075 1080 1085			3264
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cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala 1105 1110 1115 1120			3360
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aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn 1140 1145 1150			3456
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val 1155 1160 1165			3504
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Tyr	Glu	Arg	Asp 35	Glu	Gly	Asp	Lys 40	Trp	Arg	Asn	Lys	Lys 45	Phe	Glu	Leu
Gly	Leu	Glu	Phe 50	Pro	Asn	Leu 55	Pro	Tyr	Tyr	Ile	Asp 60	Gly	Asp	Val	Lys
Leu 65	Thr	Gln	Ser 70	Met	Ala	Ile 75	Ile	Arg	Tyr	Ile 75	Ala	Asp	Lys	His	Asn 80
Met	Leu	Gly	Gly 85	Cys	Pro	Lys	Glu	Arg	Ala 90	Glu	Ile	Ser	Met	Leu 95	Glu
Gly	Ala	Val	Leu 100	Asp	Ile	Arg	Tyr	Gly 105	Val	Ser	Arg	Ile	Ala 110	Tyr	Ser
Lys	Asp	Phe 115	Glu	Thr	Leu	Lys	Val 120	Asp	Phe	Leu	Ser	Lys 125	Leu	Pro	Glu
Met	Leu	Lys 130	Met	Phe	Glu	Asp 135	Arg	Leu	Cys	His	Lys 140	Thr	Tyr	Leu	Asn
Gly 145	Asp	His	Val	Thr	His 150	Pro	Asp	Phe	Met	Leu 155	Tyr	Asp	Ala	Leu	Asp 160
Val	Val	Leu	Tyr	Met 165	Asp	Pro	Met	Cys	Leu	Asp 170	Ala	Phe	Pro	Lys 175	Leu
Val	Cys	Phe 180	Lys	Lys	Arg	Ile	Glu 185	Ala	Ile	Pro	Gln	Ile	Asp 190	Lys	Tyr
Leu	Lys	Ser 195	Ser	Lys	Tyr	Ile	Ala 200	Trp	Pro	Leu	Gln	Gly 205	Trp	Gln	Ala
Thr	Phe 210	Gly	Gly	Gly	Asp 215	His	Pro	Pro	Lys	Ser	Asp 220	Leu	Val	Pro	Arg
Gly 225	Ser	Pro	Glu	Phe	Ala 230	Pro	Thr	Val	Lys	Ile	Asp 235	Ala	Gly	Met	Val 240
Val	Gly	Thr	Thr 245	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr	Val	Ser	Glu
Phe	Leu	Gly	Val 260	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe	Ala	Pro	Pro
Thr	Arg	Pro 275	Val	Pro	Trp	Ser	Thr 280	Pro	Leu	Gln	Ala	Thr	Ala	Tyr	Gly
Pro	Ala 290	Cys	Pro	Gln	Gln	Phe	Asn 295	Tyr	Pro	Glu	Glu	Leu	Arg	Glu	Ile
Thr 305	Met	Ala	Trp	Phe	Asn 310	Thr	Pro	Pro	Pro	Ser	Ala	Gly	Glu	Ser	Glu
Asp	Cys	Leu	Asn 325	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu	Asn	Thr	Asn
Lys	Ala	Val	Met 340	Val	Trp	Ile	Tyr	Gly 345	Gly	Ala	Leu	Glu	Tyr	Gly	Trp
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Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg		
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Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly		
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Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr		
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Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu		
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Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly		
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Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu		
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Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr		
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Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala		
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Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln		
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Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr		
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Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala		
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Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn		
675	680	685
Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser		
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Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr		
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Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly		
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Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val		
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Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala		
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Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys		
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Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly		
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Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys		

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Cys	Glu	Lys	Glu	Leu	900				905					910		
Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	
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Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	
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Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	
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Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	
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 bacterial expression vector pGEX-4T-1 or similar  
 vector.  
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 polylinker, 688-2163, BEST1 mature; 2164-2199,  
 spacer, 2200-3588, K:trAPAO

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 <223> gst + polylinker  
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Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
tat	gag	cgc	gat	gaa	ggg	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
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 Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr  
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0070564 043604

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Val Leu Gly Val Ala	Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val Glu
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Ala His Glu Ile Ser	Met Leu Phe Leu Thr	Asp Tyr Ile Lys Ser Ala
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Thr Gly Leu Ser Asn	Ile Phe Ser Asp Lys	Lys Asp Gly Gly Gln Tyr
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Met Arg Cys Lys Thr	Gly Met Gln Ser Ile	Cys His Ala Met Ser Lys
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Glu Leu Val Pro Gly	Ser Val His Leu Asn	Thr Pro Val Ala Glu Ile
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Glu Gln Ser Ala Ser	Gly Cys Thr Val Arg	Ser Ala Ser Gly Ala Val
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Phe Arg Ser Lys Lys	Val Val Val Ser Leu	Pro Thr Thr Leu Tyr Pro
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Thr Leu Thr Phe Ser	Pro Pro Leu Pro Ala	Glu Lys Gln Ala Leu Ala
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Glu Asn Ser Ile Leu	Gly Tyr Tyr Ser Lys	Ile Val Phe Val Trp Asp
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Lys Pro Trp Trp Arg	Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser Ser
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Cys Asp Pro Ile Ser	Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp Arg
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Gln Trp Ser Ile Thr	Cys Phe Met Val Gly	Asp Pro Gly Arg Lys Trp
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Ser Gln Gln Ser Lys	Gln Val Arg Gln Lys	Ser Val Trp Asp Gln Leu
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Arg Ala Ala Tyr Glu	Asn Ala Gly Ala Gln	Val Pro Glu Pro Ala Asn
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Val Leu Glu Ile Glu	Trp Ser Lys Gln Gln	Tyr Phe Gln Gly Ala Pro
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<220>

<223> GST:glyc(-)APAO open reading frame, 2490 nt; GST and linker, nt 1-687; Glyc (-) APAO, nt 688-2490; mutation in putative glycosylation sites in bold and underlined, nt 1288-1290 (AAT->TCC) and nt 1303-1305 (AGC->AAC).

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<222> (1)...(2487)

<221> misc\_feature

<222> (1)...(687)

<223> GST and linker

[illegible]

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Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
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tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
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Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
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Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
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Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
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Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
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Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
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Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
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Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
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Asn	Val	Ala	Ser	Pro	Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	
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Gly	Gly	Arg	Tyr	Val	Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	
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Pro	Cys	Thr	Leu	Val	Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	
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Phe	Glu	Val	Asp	Ala	Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	
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Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	
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Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	
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Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser			

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Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	
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Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	
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Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	
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Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	
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Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	
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Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	
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Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	
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Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	
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Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	
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Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	
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Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	
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Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro
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Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp
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Thr	Lys	Leu	Asn	Tyr	Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys
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Pro	Cys	Thr	Leu	Val	Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu
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Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
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Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
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Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
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Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
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Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
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Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
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													Leu



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			660						665					670			
Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser		
		675					680					685					
Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp		
		690				695					700						
Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys		
705					710					715					720		
Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln		
				725					730					735			
Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala		
			740					745					750				
Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala		
		755					760					765					
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala		
		770				775					780						
Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser		
785					790					795					800		
Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg		
			805					810						815			
Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala					
			820					825									

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